Data Augmentation to Improve the diagnosis of Melanoma using Convolutional Neural Networks

YIFAN YANG

Division of Biological Sciences, University of California, San Diego, USA Email: bjbyyf@sina.com

ABSTRACT

Early diagnosis of melanoma can substantially increase patient survival rate. Currently, dermoscopy is the dominant approach for clinical detection, but this method requires interaction with a trained clinical professional resulting in a financial burden which is a major limiting factor for many patients, especially those in remote and rural locations. It has been proposed that deep convolutional neural networks (CNNs) could allow an automated approaches for diagnosis of melanoma. However, there has been limited work regarding the use of CNNs to diagnose melanoma due to a limited amount of labelled training data available, a major limiting factor for the implementation of CNNs. This study utilises data augmentation techniques to improve CNN performance for diagnosis of melanoma, resulting a 12.4% increase in validation accuracy despite the collection of no additional training data.

CCS Concepts

• Computing methodologies~Machine learning~Machine learning approaches~Neural networks.

Additional Key Words and Phrases

Melanoma, Skin cancer, Convolutional Neural Networks (CNNs), Data augmentation

1 INTRODUCTION

Melanoma is a typical skin-related cancer, according to the NIH statistics the rate of new cases has been increasing since 1975 and currently results in approximately 75% of all skin-cancer-related deaths [1]. The 10 year survival rate of patients with melanoma detected at stage IV is 39%, increasing to 93% for patients diagnosed earlier at Stage I [2]. However, many melanoma

patients miss the opportunity for early diagnosis treatment due to the embarrassment or financial limitations preventing their access to healthcare for early diagnosis.

Historically, melanoma was diagnosed holistically by visual inspection. However, there are some deficiencies in this diagnostic approach. For example, a melanoma less than 5mm may not be detected, or some lesions could be falsely classified to benign based on ABCD rule introduced in the 1980s [4]. Dermoscopes can allow examination of melanoma in greater detail and improved diagnostic sensitivity, but this method is highly dependent on the availability of experienced clinicians. Work has been performed to develop automated classification and segmentation of melanoma from dermoscopy images, but training set sizes are limited resulting in poor performance that cannot substitute a clinical examination [5].

In the past decade, deep learning has experienced a huge revolution, deep learning enables the construction of highly generalized models inspired by the human brain's neural networks. The widely used learning architecture is the Convolutional Neural Networks (CNNs) because of the classification, segmentation, and object detection functions [6]. Image detection and classification have been applied showing strong ability of the algorithms promotes a CNN-based projection [7,8].

Machine learning techniques can provide an automated diagnosis of melanoma which could be performed at home using a smartphone appliance, matching the goal to create a quick way for patients to perform an initial check for melanoma. However, modern machine learning techniques require large amounts of training data, while the size of the current training database is limited, transformation is utilized as a data augmentation method as well as can increase the variations of datasets. The aim of this study is to examine multiple transformations to identify data augmentation techniques which improve model performance.

2 METHODS

2.1 Datasets

The dataset was extracted from Kaggle open platform¹, containing images either in .jpg or in .jpeg format, which are machine readable file formats and metadata.

¹<https://www.kaggle.com/ghulammujtaba000/melanoma-and-benign-images-only>

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BIC 2021, January 22–24, 2021, Harbin, China
© 2021 Association for Computing Machinery.
ACM ISBN 978-1-4503-9000-2/21/01...\$15.00
<https://doi.org/10.1145/3448748.3448773>

2.1.1 Data processing. The original images were stored in RGB mode, where each image has three channels: red, green and blue. Each image is defined in either benign or malignant categories which we attempt to predict with the trained model. For each image, it is defined in either benign or malignant categories. A label was assigned to each image according to the category with a certain numerical value. Here, malignant was assigned to 0, whereas benign was assigned to 1.

2.1.2 Data split. The original dataset is split into three sections, denoted as train, test and validation. The testing and validation datasets are independent from the training dataset, the testing and validation sets is used to assess model performance to ensure that the trained model is able to generalize to new data. The partition of the datasets is shown in Table 1: roughly 60% was allocated to training dataset, 20% was allocated to testing dataset, and 20% was allocated to validation dataset.

Table 1. Number of Images of each class in the training, testing, and validation set.

Class / Datasets	Train	Test	Validation
Benign	5341	1780	1781
Malignant	5341	1780	1781

2.1.3 Data normalization and augmentation. All the images were all resized and normalized utilizing the torchvision package in Python. All images were transformed to square 244 by 244 pixels. Furthermore, a range of image transformations were applied to the images. These data augmentation techniques artificially increase the diversity of the existing images by manipulating the features. Multiple transformations were performed to test the potential effects generated on the model performance.

2.2 Algorithms

The code was implemented as illustrated in the following steps:

- (1) Import all needed packages—torch, torchvision, sklearn
- (2) Transformation List²
- (3) Data Loader
 - (a) Train Loader with batch_size = 8
 - (b) Test Loader with batch_size = 50
 - (c) Validation Loader with batch_size = 50
- (4) Visualization Function

²Shown in results

- (5) Train Images Iterator
- (6) Custom CNNs Architecture³
- (7) Loop over dataset 20 times (epoch = 20)
 - (a) Training Loss
 - (b) Training F1_score
 - (c) Training Accuracy_score
 - (d) Validation Loss
 - (e) Validation F1_score
 - (f) Validation Accuracy_score

2.3 Convolutional Neural Networks Architecture

Classifying the melanoma images without an established criteria is difficult, so incorporating CNNs as a tool in the diagnosis task would be beneficial for detecting or predicting potential lesions.

There are three components that can define a basic convolutional neural network. The images loaded can be regarded as an array of pixel values. In a convolutional layer, a self-defined weight matrix will extract the certain features from the images, which run across the image so that all the pixels are covered at least once, to give a convolved output. Another component is the pooling layer. The sole purpose is to reduce the spatial size of images by compressing features relevant to prediction of the desired outcome. Pooling is done on each depth of dimension independently. Finally, after multiple layers, the output layer is used to generate an output equal to the number of classes needed. The loss function like cross-entropy is used to compute the error in prediction [9]. Using the loss function a gradient descent algorithm is applied for iterative adjustment of the model weights, which inform the convolution process, in order to minimise the calculated loss resulting in increased model performance.

2.4 Custom CNN Architecture

The custom architecture implied contains 7 layers, 2 of which are convolutional layers, 2 pooling layers and 2 linear layers, and a final output layer with two neurons representing a benign or malignant diagnosis.

The first convolutional layer has three input channels reflecting the RGB input images, generates six output channels by convolution with a (5x5) kernel, followed by a ReLU activation function, the images are passed to the first

³ More details will be introduced more in 2.4

max pooling layer, with square window of size 2 and stride value of 2. Following pooling is a second convolutional layer, six input channels are loaded from the number of output channels from the first convolutional layer. After this second convolution, sixteen output channels are produced. A kernel size of five was chosen, to be the same as the first convolutional layer. Again called by a ReLU activation function, the processed images are loaded to the second max pooling layer. All convolutional layers utilized a default stride and padding of one and zero respectively [10].

After the feature learning process, the next operation is to flatten all the output channels represented as square matrices into a one-dimensional vector. Constructing two linear layers to have a linear transformation of 2D data, finally softmax the vector before passing all the results to the output layer.

2.5 Model Performance Metrics

If the model correctly categorizes melanoma as benign, the prediction is true positive (TP); if the model correctly predicts a benign melanoma the prediction is false positive (FP). In a similar way, a false negative (FN) is the model predicts the melanoma as malignant but benign actually, and a true negative (TN) is the model correctly classifies malignant melanoma. These four primary parameters, as illustrated in Table 2, are the foundations of other measures of prediction performance.

Table 2. Primary Parameters

Model Prediction / True situation	Benign	Malignant
Benign	True Positive	False Positive
Malignant	False Negative	True Negative

The computational definition of precision is shown in equation 1, which measures the ratio of the number of images correctly classified as benign to the total number of predicted results as benign.

$$precision = \frac{TP}{TP + FP} \quad (1)$$

Recall can be calculated as illustrated in equation 2, which represents the ratio of the number of images correctly classified as benign to the total number of actual results as benign.

$$recall = \frac{TP}{TP + FN} \quad (2)$$

$$TP + FN$$

Accuracy score and F1 score are more complex than precision and recall and provides a more comprehensive measurement of model performance. The formula are displayed in equation 3 and equation 4. Accuracy score takes account the proportion of all correct predictions, while F1 score is the harmonic mean of precision and recall since sometime it is necessary to create a balance between the false positive and false negative.

$$Accuracy_score = \frac{TP + TN}{TP + TN + FP + FN} \quad (3)$$

$$F1 = 2 \cdot \frac{precision \cdot recall}{precision + recall} \quad (4)$$

3 RESULTS

No transformation is used as a referencing baseline, adding data transformations can result in increases or decreases in model performance. A random horizontal flip with a probability of 0.5, random grayscale, random crop improve the model performance dramatically. However, random horizontal flip with a probability of 0.8, and random vertical flip with a probability of 0.2 decreases the model performance (Table 5).

3.1 CNNs differentiate between malignant and benign melanoma with a F1 score of 84%

Applying total 9 distinct transformations, which the functions are explained below:

I Flip and Rotation

This group of transformations change the direction of melanoma images.

(a) Random Horizontal Flip

Flip the image horizontally with probability p

(b) Random Vertical Flip

Flip the image vertically with probability p

(c) Random Rotation

Rotate at a random angle according to the degrees

II Crop

This group of transformations change the size of melanoma images.

(a) Random Crop

Random cropping according to the given size

The parameter padding (*int*) is to set how many pixels are padded.

(b) Center Crop

Cropping from the center according to the given size

III Modify images

This group of transformations change the feature of melanoma images.

(a) Color Jitter

Randomly change the brightness, contrast and saturation of an image

(b) Random Grayscale

Converts images to grayscale with probability p

(c) Random Affine

Affine transformation

(d) Random Perspective

Performs a random perspective transformation of the given image with a given probability

The loss function is calculated with cross-entropy using pytorch, while accuracy score and F1 score through the corresponding function in Sci-Kit Learn package. Table 3 and Table 4 recorded all data from tensorboard visualization.

3.2 Horizontal flip transformation increases CNNs validation F1 score by 8.79% compared to no transformation

In Table 5 and Table 6, no transformation was set as a reference frame, the manifestations of all other transformations can be easily seen. Calculated from the following formula, all processed data are recorded in Table 5 and Table 6⁴.

$$\text{percentage_change} = \frac{\text{trans} - \text{no_trans}}{\text{no_trans}} \cdot 100\% \quad (5)$$

Table 3. Training Results

Method / Function	Ac Score	F1 Score	Loss
No trans	6.05	0.76	0.58

⁴ All data have been rounded to two decimal places.

Hori flip(0.2)	6.74	0.83	0.47
Hori flip(0.5)	6.82	0.84	0.46
Hori flip(0.8)	6.22	0.77	0.60
Vert flip(0.2)	6.21	0.77	0.60
Vert flip(0.5)	6.60	0.81	0.48
Vert flip(0.8)	6.56	0.80	0.49
Rad rotation(±90°C)	6.59	0.81	0.48
Rad grayscale	6.82	0.83	0.45
Color jitter	6.53	0.81	0.48
Rad affine	6.59	0.81	0.48
Rad perspective	6.48	0.80	0.49
Rad crop	6.79	0.83	0.46
Rad crop(pad=4)	6.65	0.82	0.48
Rad crop(pad=8)	6.53	0.79	0.48
Ctr crop(pad=4)	6.68	0.82	0.47
Ctr crop(pad=8)	6.76	0.82	0.46

Table 4. Validation Results

Method / Function	Ac Score	F1 Score	Loss
No trans	37.38	0.77	0.59
Hori flip(0.2)	41.28	0.82	0.48
Hori flip(0.5)	42.01	0.84	0.47
Hori flip(0.8)	38.16	0.78	0.61
Vert flip(0.2)	38.98	0.79	0.60
Vert flip(0.5)	40.73	0.82	0.49
Vert flip(0.8)	39.14	0.79	0.52
Rad rotation(±90°C)	41.61	0.83	0.47
Rad grayscale	41.63	0.83	0.47
Color jitter	39.61	0.80	0.50
Rad affine	41.00	0.83	0.49
Rad perspective	40.28	0.81	0.50
Rad crop	41.21	0.82	0.48
Rad crop(pad=4)	40.71	0.82	0.50
Rad crop(pad=8)	40.25	0.82	0.49
Ctr crop(pad=4)	40.70	0.82	0.49
Ctr crop(pad=8)	41.20	0.82	0.48

The best transformations are random horizontal flip with a probability of 0.5, random grayscale, and random crop, which increase the model performances by 20.70%, 20.11%, 18.87%, respectively. The worst transformations are random horizontal flip

with a probability of 0.8, and random vertical flip with a probability of 0.2, which decrease the model performances by 3.02%, 1.58%, respectively.

Table 5. Training percentage_change compared to NO trans

Method / Function	Ac Score	F1 Score	Loss
Hori flip(0.2)	+11.56%	+9.45%	-20.07%
Hori flip(0.5)	+12.87%	+10.72%	-21.53%
Hori flip(0.8)	+2.91%	+2.29%	+3.66%
Vert flip(0.2)	+2.76%	+1.73%	+3.36%
Vert flip(0.5)	+9.16%	+6.74%	-17.96%
Vert flip(0.8)	+8.57%	+5.92%	-16.41%
Rad rotation($\pm 90^\circ$ C)	+8.95%	+6.71%	-16.96%
Rad grayscale	+12.79%	+10.49%	-22.25%
Color jitter	+7.99%	+6.62%	-17.22%
Rad affine	+9.00%	+6.74%	-16.93%
Rad perspective	+7.21%	+5.32%	-15.26%
Rad crop	+12.24%	+9.93%	-21.51%
Rad crop(pad=4)	+10.06%	+8.34%	-18.33%
Rad crop(pad=8)	+8.09%	+5.20%	-17.25%
Ctr crop(pad=4)	+10.52%	+8.59%	-19.78%
Ctr crop(pad=8)	+11.75%	+8.69%	-20.86%

Table 6. Validation percentage_change compared to NO trans

Method / Function	Ac Score	F1 Score	Loss
Hori flip(0.2)	+10.43%	+6.30%	-18.38%
Hori flip(0.5)	+12.39%	+8.79%	-20.70%
Hori flip(0.8)	+2.09%	+0.92%	+3.02%
Vert flip(0.2)	+4.28%	+2.23%	+1.58%
Vert flip(0.5)	+8.96%	+6.25%	-17.45%
Vert flip(0.8)	+4.71%	+2.70%	-11.30%
Rad rotation($\pm 90^\circ$ C)	+11.32%	+8.36%	-19.57%
Rad grayscale	+11.37%	+7.99%	-20.11%
Color jitter	+5.97%	+4.12%	-15.25%
Rad affine	+9.68%	+7.61%	-17.52%
Rad perspective	+7.76%	+5.00%	-16.03%
Rad crop	+10.25%	+6.88%	-18.87%

Rad crop(pad=4)	+8.91%	+6.57%	-16.08%
Rad crop(pad=8)	+7.68%	+5.84%	-16.50%
Ctr crop(pad=4)	+8.88%	+6.60%	-17.58%
Ctr crop(pad=8)	+10.22%	+6.70%	-18.24%

Based on the calculated definitions above, the wanted result is the loss value as low as possible, and the F1 score and accuracy score as high as possible. Among all these transformations, the best three (labeled in blue) and worst three (labeled in red) are chosen.

Figure 1 gathered the best and worst results from the tensorboard visualization. Top half: Training sets. Bottom half: validation sets. Accuracy score, F1 score, loss value from left to right. X-axis and Y-axis are labeled in the graph. Each line is displayed in different color with a side annotation.

Fig. 1. Custom CNNs Architecture Results

3.3 Combining top performing transformation results combining transformations did not result in increased performance?

Further exploration of the best three transformations were done to test if multiple transformations applied together would result in further improvements in model performance. Four combinations of 2 and 3 simultaneous transformations were tested. In section 3.2, the best transformation improved the model performances by 20.70%, while the best transformation among the four new combinations improved the model performances by 20.34%. Therefore, combining the best transformation did not help to improve the model performances significantly.

Table 7. Overlay Training Results

Method / Function	Ac Score	F1 Score	Loss
Hori+grayscale	6.34	0.79	0.49
Hori+crop	6.73	0.82	0.47
grayscale+crop	6.81	0.83	0.46
Hori+gray+crop	6.65	0.81	0.47

Table 8. Overlay Validation Results

Method / Function	Ac Score	F1 Score	Loss
Hori+grayscale	38.80	0.80	0.50
Hori+crop	41.50	0.83	0.47
grayscale+crop	41.51	0.81	0.48
Hori+gray+crop	41.34	0.83	0.48

Table 9. Overlay Training percentage_change compared to NO trans

Method / Function	Ac Score	F1 Score	Loss
Hori+grayscale	+4.79%	+3.95%	-15.52%
Hori+crop	+11.24%	+7.89%	-18.97%
grayscale+crop	+12.56%	+9.21%	-20.69%
Hori+gray+crop	+9.92%	+6.58%	-18.97%

Table 10. Overlay Validation percentage_change compared to NO trans

Method / Function	Ac Score	F1 Score	Loss
Hori+grayscale	+3.80%	+3.90%	-15.25%
Hori+crop	+11.02%	+7.79%	-20.34%

grayscale+crop	+11.05%	+5.19%	-18.64%
Hori+gray+crop	+10.59%	+7.79%	-15.64%

Fig. 2. Overlay Custom CNNs Architecture Results

4 CONCLUSION AND DISCUSSION

A major limitations for the development of machine learning techniques for the diagnosis of melanoma is the limiting availability of training data which results in models with poor performance that do not generalize. In this work I have shown that data augmentation techniques improve model performance in the context of training CNNs to differentiate between malignant and benign melanoma. Random horizontal flip, random grayscale and random crop, increase the model performances significantly, while random horizontal flip with a probability of 80%, and random vertical flip with a probability of 20% downregulate the model performances.

Although I show that data augmentation techniques result in a significant increase in model performance, the accuracy achieved is too low for deployment of the these models in a clinical setting (41.51%). The purpose of this work is to assess the role of data augmentation in improving model performance which will contribute to the deployment of models in a clinical setting in the future.

The constructed CNNs (Section 2.3) utilized in this study is limited compared to larger production CNNs such as ResNet18, AlexNet, and VGG16 [11]. For future work, a comparative analysis will be conducted using the same dataset to see the difference.

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